



## SEQUENCE LISTING

<110> Fujisawa Pharmaceutical Co., Ltd  
Nakajima, Hidenori  
Nishio, Kaori  
Nishio, Nobuya  
Yoshimura, Seiji  
Ohkubo, Mitsuru

<120> Novel 35 kD Protein

<130> 260617US0

<140> 10/511,270  
<141> 2005-05-23

<150> PCT/JP03/05431  
<151> 2003-04-20

<150> Japan 2002-126107  
<151> 2002-04-26

<160> 10

<170> PatentIn version 3.3

<210> 1  
<211> 1061  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (8)..(988)

<400> 1		
gaagtct atg ctg ggt ccc caa gtc tgg tct tct gtg agg cag ggg cta		49
Met Leu Gly Pro Gln Val Trp Ser Ser Val Arg Gln Gly Leu		
1 5 10		
agc agg agc ttg tcc agg aat gtg ggg gtc tgg gcc tca ggg gag ggg		97
Ser Arg Ser Leu Ser Arg Asn Val Gly Val Trp Ala Ser Gly Glu Gly		
15 20 25 30		
aag aag gtg gac att gcg ggt atc tac ccc cct gtg acc acc ccc ttc		145
Lys Lys Val Asp Ile Ala Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe		
35 40 45		
act gcc act gca gag gtg gac tat ggg aaa ctg gag gag aat ctg cac		193
Thr Ala Thr Ala Glu Val Asp Tyr Gly Lys Leu Glu Glu Asn Leu His		
50 55 60		
aaa ctg ggc acc ttc ccc ttc cga ggc ttc gtg gtc cag ggc tcc aat		241
Lys Leu Gly Thr Phe Pro Phe Arg Gly Phe Val Val Gln Gly Ser Asn		
65 70 75		
ggc gag ttt cct ttc ctg acc agc agt gag cgc ctc gag gtg gtg agc		289
Gly Glu Phe Pro Phe Leu Thr Ser Ser Glu Arg Leu Glu Val Val Ser		
80 85 90		

cgt gtg cgc cag gcc atg ccc aag aac agg ctc ctg cta gct ggc tcc	337
Arg Val Arg Gln Ala Met Pro Lys Asn Arg Leu Leu Leu Ala Gly Ser	
95 100 105 110	
gga tgc gag tcc act caa gcc aca gtg gag atg acc gtc agc atg gcc	385
Gly Cys Glu Ser Thr Gln Ala Thr Val Glu Met Thr Val Ser Met Ala	
115 120 125	
cag gtc ggg gct gac gcg gcc atg gtg gtg acc cct tgc tac tat cgt	433
Gln Val Gly Ala Asp Ala Ala Met Val Val Thr Pro Cys Tyr Tyr Arg	
130 135 140	
ggc cgc atg agc agt gcg gcc ctc att cac cac tac acc aag gtt gct	481
Gly Arg Met Ser Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala	
145 150 155	
gat ctc tct cca atc cct gtg gtg ctg tac agt gtc cca gcc aac aca	529
Asp Leu Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Ala Asn Thr	
160 165 170	
ggg ctg gac ctg cct gtg gat gca gtg gtc acg ctt tcc cag cac ccg	577
Gly Leu Asp Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro	
175 180 185 190	
aat att gtg ggc atg aag gac agc ggt ggt gat gtg acc agg att ggg	625
Asn Ile Val Gly Met Lys Asp Ser Gly Gly Asp Val Thr Arg Ile Gly	
195 200 205	
ctg att gtt cac aag acc agg aag cag gat ttt cag gtg ttg gct gga	673
Leu Ile Val His Lys Thr Arg Lys Gln Asp Phe Gln Val Leu Ala Gly	
210 215 220	
tcg gct ggc ttt ctg atg gcc agc tat gcc ttg gga gct gtg ggg ggc	721
Ser Ala Gly Phe Leu Met Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly	
225 230 235	
gtc tgc gcc ctg gcc aat gtc ctg ggg gct cag gtg tgc cag ctg gag	769
Val Cys Ala Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu	
240 245 250	
cga ctg tgc tgc acg ggg caa tgg gaa gat gcc cag aaa ctg cag cac	817
Arg Leu Cys Cys Thr Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His	
255 260 265 270	
cgc ctc att gag cca aac gct gcg gtg acc cgg cgc ttt ggg atc cca	865
Arg Leu Ile Glu Pro Asn Ala Ala Val Thr Arg Arg Phe Gly Ile Pro	
275 280 285	
ggg ctg aag aaa atc atg gac tgg ttt ggc tac tat gga ggc ccc tgc	913
Gly Leu Lys Lys Ile Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys	
290 295 300	
cgc gcc ccc ttg cag gag ctg agc ccc gct gag gag gag gca ctg cgc	961
Arg Ala Pro Leu Gln Glu Leu Ser Pro Ala Glu Glu Ala Leu Arg	
305 310 315	
atg gat ttc acc agc aac ggc tgg ctc tgagggcagg cagggtccat	1008
Met Asp Phe Thr Ser Asn Gly Trp Leu	
320 325	
ggctggcctg agcccatctc agcctcctgc cttgcacttg cagcctgaat tcc	1061

<210> 2  
<211> 327  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Leu Gly Pro Gln Val Trp Ser Ser Val Arg Gln Gly Leu Ser Arg  
1 5 10 15

Ser Leu Ser Arg Asn Val Gly Val Trp Ala Ser Gly Glu Gly Lys Lys  
20 25 30

Val Asp Ile Ala Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala  
35 40 45

Thr Ala Glu Val Asp Tyr Gly Lys Leu Glu Glu Asn Leu His Lys Leu  
50 55 60

Gly Thr Phe Pro Phe Arg Gly Phe Val Val Gln Gly Ser Asn Gly Glu  
65 70 75 80

Phe Pro Phe Leu Thr Ser Ser Glu Arg Leu Glu Val Val Ser Arg Val  
85 90 95

Arg Gln Ala Met Pro Lys Asn Arg Leu Leu Leu Ala Gly Ser Gly Cys  
100 105 110

Glu Ser Thr Gln Ala Thr Val Glu Met Thr Val Ser Met Ala Gln Val  
115 120 125

Gly Ala Asp Ala Ala Met Val Val Thr Pro Cys Tyr Tyr Arg Gly Arg  
130 135 140

Met Ser Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala Asp Leu  
145 150 155 160

Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Ala Asn Thr Gly Leu  
165 170 175

Asp Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro Asn Ile  
180 185 190

Val Gly Met Lys Asp Ser Gly Gly Asp Val Thr Arg Ile Gly Leu Ile  
195 200 205

Val His Lys Thr Arg Lys Gln Asp Phe Gln Val Leu Ala Gly Ser Ala  
210 215 220

Gly Phe Leu Met Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly Val Cys  
225 230 235 240

Ala Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu  
245 250 255

Cys Cys Thr Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His Arg Leu  
260 265 270

Ile Glu Pro Asn Ala Ala Val Thr Arg Arg Phe Gly Ile Pro Gly Leu  
275 280 285

Lys Lys Ile Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala  
290 295 300

Pro Leu Gln Glu Leu Ser Pro Ala Glu Glu Ala Leu Arg Met Asp  
305 310 315 320

Phe Thr Ser Asn Gly Trp Leu  
325

<210> 3  
<211> 1017  
<212> DNA  
<213> Rattus sp.

<220>  
<221> CDS  
<222> (9)..(1016)

<400> 3  
cgggatcc atg ctg ggc ccc caa atc tgg gcc tcc atg agg cag ggg ctg 50  
Met Leu Gly Pro Gln Ile Trp Ala Ser Met Arg Gln Gly Leu  
1 5 10

agc agg ggc ttg tct agg aac gtg aag ggg aag aag ata gac att gcc 98  
Ser Arg Gly Leu Ser Arg Asn Val Lys Gly Lys Lys Ile Asp Ile Ala  
15 20 25 30

ggc atc tac cca ccc gtg acc acc cca ttc acc gcc acc gca gaa gta 146  
Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala Thr Ala Glu Val  
35 40 45

gac tat ggg aaa ctg gaa gag aac ctg aac aaa ctg gcc gcc ttc ccc 194  
Asp Tyr Gly Lys Leu Glu Glu Asn Leu Asn Lys Leu Ala Ala Phe Pro  
50 55 60

ttt cga ggc ttc gtg gtc cag ggc tct act gga gag ttt cca ttc ctg 242  
Phe Arg Gly Phe Val Val Gln Gly Ser Thr Gly Glu Phe Pro Phe Leu

65	70	75	
acc agc ctt gag cgc cta gag gtg gtg	agc cga gtg cgc cag gcc ata		290
Thr Ser Leu Glu Arg Leu Glu Val Val Ser Arg Val Arg Gln Ala Ile			
80	85	90	
ccc aag gac aag ctc ctg ata gcc ggc tct ggc tgc gag tcc acg caa			338
Pro Lys Asp Lys Leu Leu Ile Ala Gly Ser Gly Cys Glu Ser Thr Gln			
95	100	105	110
gcc aca gta gag atg act gtc agc atg gct cag gtg ggt gct gat gcc			386
Ala Thr Val Glu Met Thr Val Ser Met Ala Gln Val Gly Ala Asp Ala			
115	120	125	
gcc atg gtg gtg acc cct tgt tac tat cgc ggc cgc atg aac agc gct			434
Ala Met Val Thr Pro Cys Tyr Tyr Arg Gly Arg Met Asn Ser Ala			
130	135	140	
gcc ctc att cac cac tac acc aag gtt gct gat ctt tct cca atc ccg			482
Ala Leu Ile His His Tyr Thr Lys Val Ala Asp Leu Ser Pro Ile Pro			
145	150	155	
gtg gtg ctg tac agt gtc cca ggc aac acg ggt cta gag ctg cct gtg			530
Val Val Leu Tyr Ser Val Pro Gly Asn Thr Gly Leu Glu Leu Pro Val			
160	165	170	
gat gcc gtg gtc aca ttg tct cag cac cca aat atc att ggc ttg aag			578
Asp Ala Val Val Thr Leu Ser Gln His Pro Asn Ile Ile Gly Leu Lys			
175	180	185	190
gac agt ggt gga gat gtg acc agg act ggg ctg att gtt cac aag acc			626
Asp Ser Gly Gly Asp Val Thr Arg Thr Gly Leu Ile Val His Lys Thr			
195	200	205	
agc aag cag gat ttc cag gtg ttg gct ggg tca gtt ggc ttc ctc ctg			674
Ser Lys Gln Asp Phe Gln Val Leu Ala Gly Ser Val Gly Phe Leu Leu			
210	215	220	
gcc agc tat gct gga gct gtt ggg ggc ata tgt ggc ctg gcc aat			722
Ala Ser Tyr Ala Val Gly Ala Val Gly Gly Ile Cys Gly Leu Ala Asn			
225	230	235	
gtc ttg ggg gcc cag gtg tgc cag ctg gag aga ctc tgc ctc aca ggg			770
Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu Cys Leu Thr Gly			
240	245	250	
cag ggg gaa gct gcc cag aga ctg cag cac cgc ctc atc gag ccc aac			818
Gln Gly Glu Ala Ala Gln Arg Leu Gln His Arg Leu Ile Glu Pro Asn			
255	260	265	270
act gcg gtg acc cgg cgc ttt gga ata cca ggg ctg aag aaa acc atg			866
Thr Ala Val Thr Arg Arg Phe Gly Ile Pro Gly Leu Lys Lys Thr Met			
275	280	285	
gac tgg ttt ggc tac tat gga ggt ccc tgc cgt gcc ccc ttg cag gag			914
Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala Pro Leu Gln Glu			
290	295	300	
ttg agc ccc tca gag gaa gag gcg ctt cgc ttg gat ttc agc aac aat			962
Leu Ser Pro Ser Glu Glu Ala Leu Arg Leu Asp Phe Ser Asn Asn			
305	310	315	

ggc tgg ctt taa tga caa gcg ggg gac acc tgg tct gag ctg tct cag 1010  
Gly Trp Leu Gln Ala Gly Asp Thr Trp Ser Glu Leu Ser Gln  
320 325 330

aat tcc g 1017  
Asn Ser

<210> 4  
<211> 321  
<212> PRT  
<213> Rattus sp.

<400> 4

Met Leu Gly Pro Gln Ile Trp Ala Ser Met Arg Gln Gly Leu Ser Arg  
1 5 10 15

Gly Leu Ser Arg Asn Val Lys Gly Lys Lys Ile Asp Ile Ala Gly Ile  
20 25 30

Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala Thr Ala Glu Val Asp Tyr  
35 40 45

Gly Lys Leu Glu Glu Asn Leu Asn Lys Leu Ala Ala Phe Pro Phe Arg  
50 55 60

Gly Phe Val Val Gln Gly Ser Thr Gly Glu Phe Pro Phe Leu Thr Ser  
65 70 75 80

Leu Glu Arg Leu Glu Val Val Ser Arg Val Arg Gln Ala Ile Pro Lys  
85 90 95

Asp Lys Leu Leu Ile Ala Gly Ser Gly Cys Glu Ser Thr Gln Ala Thr  
100 105 110

Val Glu Met Thr Val Ser Met Ala Gln Val Gly Ala Asp Ala Ala Met  
115 120 125

Val Val Thr Pro Cys Tyr Tyr Arg Gly Arg Met Asn Ser Ala Ala Leu  
130 135 140

Ile His His Tyr Thr Lys Val Ala Asp Leu Ser Pro Ile Pro Val Val  
145 150 155 160

Leu Tyr Ser Val Pro Gly Asn Thr Gly Leu Glu Leu Pro Val Asp Ala  
165 170 175

Val Val Thr Leu Ser Gln His Pro Asn Ile Ile Gly Leu Lys Asp Ser  
180 185 190

Gly Gly Asp Val Thr Arg Thr Gly Leu Ile Val His Lys Thr Ser Lys  
195 200 205

Gln Asp Phe Gln Val Leu Ala Gly Ser Val Gly Phe Leu Leu Ala Ser  
210 215 220

Tyr Ala Val Gly Ala Val Gly Gly Ile Cys Gly Leu Ala Asn Val Leu  
225 230 235 240

Gly Ala Gln Val Cys Gln Leu Glu Arg Leu Cys Leu Thr Gly Gln Gly  
245 250 255

Glu Ala Ala Gln Arg Leu Gln His Arg Leu Ile Glu Pro Asn Thr Ala  
260 265 270

Val Thr Arg Arg Phe Gly Ile Pro Gly Leu Lys Lys Thr Met Asp Trp  
275 280 285

Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala Pro Leu Gln Glu Leu Ser  
290 295 300

Pro Ser Glu Glu Glu Ala Leu Arg Leu Asp Phe Ser Asn Asn Gly Trp  
305 310 315 320

Leu

<210> 5  
<211> 13  
<212> PRT  
<213> Rattus sp.

<400> 5

Gln Ala Gly Asp Thr Trp Ser Glu Leu Ser Gln Asn Ser  
1 5 10

<210> 6  
<211> 202  
<212> PRT  
<213> Rattus sp.

<220>  
<221> MISC\_FEATURE  
<222> (165)..(165)  
<223> Xaa can be any naturally occurring amino acid

<400> 6

Gly Arg Met Asn Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala  
1 5 10 15

Asp Leu Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Gly Asn Thr  
20 25 30

Gly Leu Glu Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro  
35 40 45

Asn Ile Ile Gly Leu Lys Asp Ser Gly Gly Asp Val Thr Arg Thr Gly  
50 55 60

Leu Ile Val His Lys Thr Ser Lys Gln Asp Phe Gln Val Leu Ala Gly  
65 70 75 80

Ser Val Gly Phe Leu Leu Ala Ser Tyr Ala Val Gly Ala Val Gly Gly  
85 90 95

Ile Val Gly Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu  
100 105 110

Arg Leu Cys Leu Thr Gly Gln Gly Glu Ala Ala Gln Arg Leu Gln His  
115 120 125

Arg Leu Ile Glu Pro Asn Thr Ala Val Thr Arg Arg Phe Gly Ile Pro  
130 135 140

Gly Leu Lys Lys Thr Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys  
145 150 155 160

Arg Ala Pro Leu Xaa Glu Leu Ser Pro Ser Glu Glu Ala Leu Arg  
165 170 175

Leu Asp Phe Ser Asn Asn Gly Trp Leu Gln Ala Gly Asp Thr Trp Ser  
180 185 190

Glu Leu Ser Gln Thr Leu Val Pro Thr Val  
195 200

<210> 7

<211> 30

<212> DNA

<213> Rattus sp.

<400> 7

cgggatccaa tgctgggccc ccaaattctgg

30

<210> 8  
<211> 24  
<212> DNA  
<213> Rattus sp.

<400> 8  
cggaattctg agacagctca gacc

24

<210> 9  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 9  
gaagatctat gctgggtccc caagtctgg

29

<210> 10  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 10  
ggaattcagg ctgcaagtgc aaggcaggag

30